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METHODS FOR IMMUNOSUPPRESSIVE AGENTS****Group Art Unit: 1634****Our Reference No.: SUPP-P05-008**

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## SEQUENCE LISTING

<110> Crabtree, Gerald R.  
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<120> NF-AT POLYPEPTIDES AND POLYNUCLEOTIDES AND SCREENING  
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<130> APV-008.04

<140> 09/232,346

<141> 1999-01-15

<150> 08/507,032

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<150> 08/228,944

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<151> 1994-06-13

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gaggagaaac tttggggccc ggcgcggcg cggcgccac catgaagtca gggaggaag 3117  
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cggaccacco ctcggggtac ggagcagctt tggacgggtg gcccgcggc tacttctct 3297  
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ctcgtgctt gggcctgtac cacaacaata accagtttt ccacgatgtg gaggtggaag 3417  
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actcagaggc ctctcctac gactccact actcgtacc gtacgcgtcc cccagacgt 3597  
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gcgggctggg ggcctgcaca ctgctgggtt cccgcagca ctccctcc accctgcccc 3717  
gcgcagcgt cactgaggag agctgggtg gtgcccgtc ctccagacc ggttccctt 3777  
gcaacaagag gaagtacagc ctcaacggc ggcagccgc ctactcccc caccactgc 3837  
ccacgcgtc cccgcaggg tccccaggg tcagcgtgac cgaagactcg tggttgggca 3897  
acaccacca gtaccagc tcggccatcg tggccgcat caacgagctg accaccgaca 3957  
gcgcctgga cctgggagat ggcgtccctg tcaagtccg caagaccacc ctggagcagc 4017

15

agccctcagt ggcgctcaag gtggagcccg tcggggagga cctgggcagc ccccccgc 4077  
 cgcccgactt cgcgcccga gactactcct ctttcagca catcaggaag ggcggcttct 4137  
 gcgaccagta cctggcggtg ccgcagcacc cctaccagtg ggcgaaagccc aagcccctgt 4197  
 cccctacgtc ctacatgagc ccgaccctgc ccgcccctga ctggcagctg cegtccact 4257  
 cagggccgta tgagcttcgg attgaggtgc agcccagtc ccaccacga gccactacg 4317  
 agacggaggg cagccggggg gcagtgaagg cgtcgccggg aggacacccc atcgtgcagc 4377  
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 cgagaacag catgcgagcc gtcattgact gtgccggaat cctgaaactc agaaactcgg 4617  
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 ttccggaatca gaggataacc agcccgttc acgtcagttt ctacgtctgc aacgggaaga 5037  
 gaaagggag ccagtaccag cgtttcacct acctcccg caacggtaac gccatctttc 5097  
 taaccgtaag ccgtgaacat gagcgctgg ggtgctttt ctaaagacgc agaaacgacg 5157  
 tcgcgtaaa gcagcgtggc gtgttgca ca ttaactgtg tgatgtcccg ttagtgagac 5217  
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 tccctgttgg ggggtggggg cgggggttgc ataotcagat agtcacgggtt attttgcctc 5337  
 ttgcgaatgt ataacagcca aggggaaaac atggctcttc tgctccaaa aactgagggg 5397  
 gtccgtgtgt gcatttgac cctaaagctg cttacggtga aaaggcaa at aggtatagct 5457  
 attttgcagg cacccttagg aataaacttt gcttttaaaa aaaa 5502

<210> 46  
 <211> 716  
 <212> PRT  
 <213> human

<400> 46

Met Pro Ser Thr Ser Phe Pro Val Pro Ser Lys Phe Pro Leu Gly Pro

1

5

10

15

16

Glu Ala Ala Val Phe Gly Arg Gly Glu Thr Leu Gly Pro Ala Pro Arg  
 20 25 30  
 Ala Gly Gly Thr Met Lys Ser Ala Glu Glu Glu His Tyr Gly Tyr Ala  
 35 40 45  
 Ser Ser Asn Val Ser Pro Ala Leu Pro Leu Pro Thr Ala His Ser Thr  
 50 55 60  
 Leu Pro Ala Pro Cys His Asn Leu Gln Thr Ser Thr Pro Gly Ile Ile  
 65 70 75 80  
 Pro Pro Ala Asp His Pro Ser Gly Tyr Gly Ala Ala Leu Asp Gly Gly  
 85 90 95  
 Pro Ala Gly Tyr Phe Leu Ser Ser Gly His Thr Arg Pro Asp Arg Ala  
 100 105 110  
 Pro Ala Leu Glu Ser Pro Arg Ile Glu Ile Thr Ser Cys Leu Gly Leu  
 115 120 125  
 Tyr His Asn Asn Asn Gln Phe Phe His Asp Val Glu Val Glu Asp Val  
 130 135 140  
 Leu Pro Ser Ser Lys Arg Ser Pro Ser Thr Ala Thr Leu Ser Leu Pro  
 145 150 155 160  
 Ser Leu Glu Ala Tyr Arg Asp Pro Ser Cys Leu Ser Pro Ala Ser Ser  
 165 170 175  
 Leu Ser Ser Arg Ser Cys Asn Ser Glu Ala Ser Ser Tyr Glu Ser Asn  
 180 185 190  
 Tyr Ser Tyr Pro Tyr Ala Ser Pro Gln Thr Ser Pro Trp Gln Ser Pro  
 195 200 205  
 Cys Val Ser Pro Lys Thr Thr Asp Pro Glu Glu Gly Phe Pro Arg Gly  
 210 215 220  
 Leu Gly Ala Cys Thr Leu Leu Gly Ser Pro Gln His Ser Pro Ser Thr  
 225 230 235 240  
 Ser Pro Arg Ala Ser Val Thr Glu Glu Ser Trp Leu Gly Ala Arg Ser  
 245 250 255  
 Ser Arg Pro Ala Ser Pro Cys Asn Lys Arg Lys Tyr Ser Leu Asn Gly  
 260 265 270  
 Arg Gln Pro Pro Tyr Ser Pro His His Ser Pro Thr Pro Ser Pro His  
 275 280 285  
 Gly Ser Pro Arg Val Ser Val Thr Asp Asp Ser Trp Leu Gly Asn Thr  
 290 295 300  
 Thr Gln Tyr Thr Ser Ser Ala Ile Val Ala Ala Ile Asn Glu Leu Thr  
 305 310 315 320  
 Thr Asp Ser Ser Leu Asp Leu Gly Asp Gly Val Pro Val Lys Ser Arg  
 325 330 335

17

Lys Thr Thr Leu Glu Gln Gln Pro Ser Val Ala Leu Lys Val Glu Pro  
 340 345 350  
 Val Gly Glu Asp Leu Gly Ser Pro Pro Pro Pro Ala Asp Phe Ala Pro  
 355 360 365  
 Glu Asp Tyr Ser Ser Phe Gln His Ile Arg Lys Gly Gly Phe Cys Asp  
 370 375 380  
 Gln Tyr Leu Ala Val Pro Gln His Pro Tyr Gln Trp Ala Lys Pro Lys  
 385 390 395 400  
 Pro Leu Ser Pro Thr Ser Tyr Met Ser Pro Thr Leu Pro Ala Leu Asp  
 405 410 415  
 Trp Gln Leu Pro Ser His Ser Gly Pro Tyr Glu Leu Arg Ile Glu Val  
 420 425 430  
 Gln Pro Lys Ser His His Arg Ala His Tyr Glu Thr Glu Gly Ser Arg  
 435 440 445  
 Gly Ala Val Lys Ala Ser Ala Gly Gly His Pro Ile Val Gln Leu His  
 450 455 460  
 Gly Tyr Leu Glu Asn Glu Pro Leu Met Leu Gln Leu Phe Ile Gly Thr  
 465 470 475 480  
 Ala Asp Asp Arg Leu Leu Arg Pro His Ala Phe Tyr Gln Val His Arg  
 485 490 495  
 Ile Thr Gly Lys Thr Val Ser Thr Thr Ser His Glu Ala Ile Leu Ser  
 500 505 510  
 Asn Thr Lys Val Leu Glu Ile Pro Leu Leu Pro Glu Asn Ser Met Arg  
 515 520 525  
 Ala Val Ile Asp Cys Ala Gly Ile Leu Lys Leu Arg Asn Ser Asp Ile  
 530 535 540  
 Glu Leu Arg Lys Gly Glu Thr Asp Ile Gly Arg Lys Asn Thr Arg Val  
 545 550 555 560  
 Arg Leu Val Phe Arg Val His Val Pro Gln Pro Ser Gly Arg Thr Leu  
 565 570 575  
 Ser Leu Gln Val Ala Ser Asn Pro Ile Glu Cys Ser Gln Arg Ser Ala  
 580 585 590  
 Gln Glu Leu Pro Leu Val Glu Lys Gln Ser Thr Asp Ser Tyr Pro Val  
 595 600 605  
 Val Gly Gly Lys Lys Met Val Leu Ser Gly His Asn Phe Leu Gln Asp  
 610 615 620  
 Ser Lys Val Ile Phe Val Glu Lys Ala Pro Asp Gly His His Val Trp  
 625 630 635 640  
 Glu Met Glu Ala Lys Thr Asp Arg Asp Leu Cys Lys Pro Asn Ser Leu  
 645 650 655

18

Val Val Glu Ile Pro Pro Phe Arg Asn Gln Arg Ile Thr Ser Pro Val  
660 665 670

His Val Ser Phe Tyr Val Cys Asn Gly Lys Arg Lys Gly Ser Gln Tyr  
675 680 685

Gln Arg Phe Thr Tyr Leu Pro Ala Asn Gly Asn Ala Ile Phe Leu Thr  
690 695 700

Val Ser Arg Glu His Glu Arg Val Gly Cys Phe Phe  
705 710 715

<210> 47  
<211> 302  
<212> PRT  
<213> Drosophila

<400> 47  
Thr Lys Asn Val Arg Lys Lys Pro Tyr Val Lys Ile Thr Glu Gln Pro  
1 5 10 15

Ala Gly Lys Ala Leu Arg Phe Arg Tyr Glu Cys Glu Gly Arg Ser Ala  
20 25 30

Gly Ser Ile Pro Gly Val Asn Ser Thr Pro Glu Asn Lys Thr Tyr Pro  
35 40 45

Thr Ile Glu Ile Val Gly Tyr Lys Gly Arg Ala Val Val Val Val Ser  
50 55 60

Cys Val Thr Lys Asp Thr Pro Tyr Arg Pro His Pro His Asn Leu Val  
65 70 75 80

Gly Lys Glu Gly Cys Lys Lys Gly Val Cys Thr Leu Glu Ile Asn Ser  
85 90 95

Glu Thr Met Arg Ala Val Phe Ser Asn Leu Gly Ile Gln Cys Val Lys  
100 105 110

Lys Lys Asp Ile Glu Ala Ala Leu Lys Ala Arg Glu Glu Ile Arg Val  
115 120 125

Asp Pro Phe Lys Thr Gly Phe Ser His Arg Phe Gln Pro Ser Ser Ile  
130 135 140

Asp Leu Asn Ser Val Arg Leu Cys Phe Gln Val Phe Met Glu Ser Glu  
145 150 155 160

Gln Lys Gly Arg Phe Thr Ser Pro Leu Pro Pro Val Val Ser Glu Pro  
165 170 175

Ile Phe Asp Lys Lys Ala Met Ser Asp Leu Val Ile Cys Arg Leu Cys  
180 185 190

Ser Cys Ser Ala Thr Val Phe Gly Asn Thr Gln Ile Ile Leu Leu Cys  
195 200 205

Glu Lys Val Ala Lys Glu Asp Ile Ser Val Arg Phe Phe Glu Glu Lys  
210 215 220

19

Asn Gly Gln Ser Val Trp Glu Ala Phe Gly Asp Phe Gln His Thr Asp  
225 230 235 240

Val His Lys Gln Thr Ala Ile Thr Phe Lys Thr Pro Arg Tyr His Thr  
245 250 255

Leu Asp Ile Thr Glu Pro Ala Lys Val Phe Ile Gln Leu Arg Arg Pro  
260 265 270

Ser Asp Gly Val Thr Ser Glu Ala Leu Pro Phe Glu Tyr Val Pro Met  
275 280 285

Asp Ser Asp Pro Ala His Leu Arg Arg Lys Arg Gln Lys Thr  
290 295 300

&lt;210&gt; 48

&lt;211&gt; 296

&lt;212&gt; PRT

&lt;213&gt; human

&lt;400&gt; 48

Met Ala Ser Gly Leu Tyr Asn Pro Tyr Ile Glu Ile Ile Glu Gln Pro  
1 5 10 15

Arg Gln Arg Gly Met Arg Phe Arg Tyr Lys Cys Glu Gly Arg Ser Ala  
20 25 30

Gly Ser Ile Pro Gln Glu His Ser Thr Asp Asn Asn Arg Thr Tyr Pro  
35 40 45

Ser Ile Asn Ile Met Asn Tyr Tyr Gly Arg Gly Lys Val Arg Ile Thr  
50 55 60

Leu Val Thr Lys Asn Asp Pro Tyr Lys Pro His Pro His Asp Leu Val  
65 70 75 80

Gly Lys Asp Cys Arg Asp Gly Tyr Tyr Glu Ala Glu Phe Gly Asn Glu  
85 90 95

Arg Arg Pro Leu Phe Phe Gln Asn Leu Gly Ile Arg Cys Val Lys Lys  
100 105 110

Lys Glu Val Lys Glu Ala Ile Ile Thr Arg Ile Lys Ala Gly Ile Asn  
115 120 125

Pro Phe Asn Val Pro Glu Lys Gln Leu Asn Asp Ile Glu Asp Cys Asp  
130 135 140

Leu Asn Val Val Arg Leu Cys Phe Gln Val Phe Leu Pro Asp Glu His  
145 150 155 160

Gly Asn Leu Thr Thr Ala Leu Pro Pro Val Val Ser Asn Pro Ile Tyr  
165 170 175

Asp Asn Arg Ala Pro Asn Thr Ala Glu Leu Arg Ile Cys Arg Val Asn  
180 185 190

Lys Asn Cys Gly Ser Val Arg Gly Gly Asp Glu Ile Phe Leu Leu Cys  
195 200 205

20

Asp Lys Val Gln Lys Asp Asp Ile Glu Val Arg Phe Val Leu Asn Asp  
210 215 220

Trp Glu Ala Lys Gly Ile Phe Ser Gln Ala Asp Val His Arg Gln Val  
225 230 235 240

Ala Ile Val Phe Lys Thr Pro Pro Tyr Cys Lys Ala Ile Thr Glu Pro  
245 250 255

Val Thr Val Lys Met Gln Leu Arg Arg Pro Ser Asp Gln Glu Val Ser  
260 265 270

Glu Ser Met Asp Phe Arg Tyr Leu Pro Asp Glu Lys Asp Thr Tyr Gly  
275 280 285

Asn Lys Ala Lys Lys Gln Lys Thr  
290 295

<210> 49  
<211> 332  
<212> PRT  
<213> human

<400> 49  
Ile Pro Leu Ser Thr Asp Gly Pro Tyr Leu Gln Ile Leu Glu Gln Pro  
1 5 10 15

Lys Gln Arg Gly Phe Arg Phe Arg Tyr Val Cys Glu Gly Pro Ser His  
20 25 30

Gly Gly Leu Pro Gly Ala Ser Ser Glu Lys Asn Lys Lys Ser Tyr Pro  
35 40 45

Gln Val Lys Ile Cys Asn Tyr Val Gly Pro Ala Lys Val Ile Val Gln  
50 55 60

Leu Val Thr Asn Gly Lys Asn Ile His Leu His Ala His Ser Leu Val  
65 70 75 80

Gly Lys His Cys Glu Asp Gly Val Cys Thr Val Thr Ala Gly Pro Lys  
85 90 95

Asp Met Val Val Gly Phe Ala Asn Leu Gly Ile Leu His Val Thr Lys  
100 105 110

Lys Lys Val Phe Glu Thr Leu Glu Ala Arg Met Thr Glu Ala Cys Ile  
115 120 125

Arg Gly Tyr Asn Pro Gly Leu Leu Val His Ser Asp Leu Ala Tyr Leu  
130 135 140

Gln Ala Glu Gly Gly Gly Asp Arg Gln Leu Thr Asp Arg Glu Lys Glu  
145 150 155 160

Ile Ile Arg Gln Ala Ala Val Gln Gln Thr Lys Glu Met Asp Leu Ser  
165 170 175

Val Val Arg Leu Met Phe Thr Ala Phe Leu Pro Asp Ser Thr Gly Ser  
180 185 190

21

Phe Thr Arg Arg Leu Glu Pro Val Val Ser Asp Ala Ile Tyr Asp Ser  
195 200 205

Lys Ala Pro Asn Ala Ser Asn Leu Lys Ile Val Arg Met Asp Arg Thr  
210 215 220

Ala Gly Cys Val Thr Gly Gly Glu Glu Ile Tyr Leu Leu Cys Asp Lys  
225 230 235 240

Val Gln Lys Asp Asp Ile Gln Ile Arg Phe Tyr Glu Glu Glu Glu Asn  
245 250 255

Gly Gly Val Trp Glu Gly Phe Gly Asp Phe Ser Pro Thr Asp Val His  
260 265 270

Arg Gln Phe Ala Ile Val Phe Lys Thr Pro Lys Tyr Lys Asp Val Asn  
275 280 285

Ile Thr Lys Pro Ala Ser Val Phe Val Gln Leu Arg Arg Lys Ser Asp  
290 295 300

Leu Glu Thr Ser Glu Pro Lys Pro Phe Leu Tyr Tyr Pro Glu Ile Lys  
305 310 315 320

Asp Lys Glu Glu Val Gln Arg Lys Arg Gln Lys Leu  
325 330

<210> 50  
<211> 295  
<212> PRT  
<213> human

<400> 50  
Glu Pro Ala Gln Ala Ser Gly Pro Tyr Val Glu Ile Ile Glu Gln Pro  
1 5 10 15

Lys Gln Arg Gly Met Arg Phe Arg Tyr Lys Cys Glu Gly Arg Ser Ala  
20 25 30

Gly Ser Ile Pro Gly Glu Arg Ser Thr Asp Thr Thr Lys Thr His Pro  
35 40 45

Thr Ile Lys Ile Asn Gly Tyr Thr Gly Pro Gly Thr Val Arg Ile Ser  
50 55 60

Leu Val Thr Lys Asp Pro Pro His Arg Pro His Pro His Glu Leu Val  
65 70 75 80

Gly Lys Asp Cys Arg Asp Gly Tyr Tyr Glu Ala Asp Leu Cys Pro Asp  
85 90 95

Arg Asp Ser Ile His Ser Phe Gln Asn Leu Gly Ile Gln Cys Val Lys  
100 105 110

Lys Arg Asp Leu Glu Gln Ala Ile Ser Gln Arg Ile Gln Thr Asn Asn  
115 120 125

Asn Pro Phe His Val Pro Ile Glu Glu Gln Arg Gly Asp Tyr Asp Leu  
130 135 140

22

Asn Ala Val Arg Leu Cys Phe Gln Val Thr Val Arg Asp Pro Ala Gly  
 145 150 155 160  
 Arg Pro Leu Leu Leu Thr Pro Val Leu Ser His Pro Ile Phe Asp Asn  
 165 170 175  
 Arg Ala Pro Asn Thr Ala Glu Leu Lys Ile Cys Arg Val Asn Arg Asn  
 180 185 190  
 Ser Gly Ser Cys Leu Gly Gly Asp Glu Ile Phe Leu Leu Cys Asp Lys  
 195 200 205  
 Val Gln Lys Glu Asp Ile Glu Val Tyr Phe Thr Gly Pro Gly Trp Glu  
 210 215 220  
 Ala Arg Gly Ser Phe Ser Gln Ala Asp Val His Arg Gln Val Ala Ile  
 225 230 235 240  
 Val Phe Arg Thr Pro Pro Tyr Ala Asp Pro Ser Leu Gln Ala Pro Val  
 245 250 255  
 Arg Val Ser Met Gln Leu Arg Arg Pro Ser Asp Arg Glu Leu Ser Glu  
 260 265 270  
 Pro Met Glu Phe Gln Tyr Leu Pro Asp Thr Asp Asp Arg His Arg Ile  
 275 280 285  
 Glu Glu Lys Arg Lys Arg Thr  
 290 295  
  
 <210> 51  
 <211> 293  
 <212> PRT  
 <213> human  
  
 <400> 51  
 Gln Leu Pro Ser His Ser Gly Pro Tyr Glu Leu Arg Ile Glu Val Gln  
 1 5 10 15  
 Pro Lys Ser His His Arg Ala His Tyr Glu Thr Glu Gly Ser Arg Gly  
 20 25 30  
 Ala Val Lys Ala Ser Ala Gly Gly His Pro Ile Val Gln Leu His Gly  
 35 40 45  
 Tyr Leu Glu Asn Glu Pro Leu Met Leu Gln Leu Phe Ile Gly Thr Ala  
 50 55 60  
 Asp Asp Arg Leu Leu Arg Pro His Ala Phe Tyr Gln Val His Arg Ile  
 65 70 75 80  
 Thr Gly Lys Thr Val Ser Thr Thr Ser His Glu Ala Ile Leu Ser Asn  
 85 90 95  
 Thr Lys Val Leu Glu Ile Pro Leu Leu Pro Glu Asn Ser Met Arg Ala  
 100 105 110  
 Val Ile Asp Cys Ala Gly Ile Leu Lys Leu Arg Asn Ser Asp Ile Glu  
 115 120 125

23

Leu Arg Lys Gly Glu Thr Asp Ile Gly Arg Lys Asn Thr Arg Val Arg  
 130 135 140  
 Leu Val Phe Arg Val His Val Pro Gln Pro Ser Gly Arg Thr Leu Ser  
 145 150 155 160  
 Leu Gln Val Ala Ser Asn Pro Ile Glu Cys Ser Gln Arg Ser Ala Gln  
 165 170 175  
 Glu Leu Pro Leu Val Glu Lys Gln Ser Thr Asp Ser Tyr Pro Val Val  
 180 185 190  
 Gly Gly Lys Lys Met Val Leu Ser Gly His Asn Phe Leu Gln Asp Ser  
 195 200 205  
 Lys Val Ile Phe Val Glu Lys Ala Pro Asp Gly His His Val Trp Glu  
 210 215 220  
 Met Glu Ala Lys Thr Asp Arg Asp Leu Cys Lys Pro Asn Ser Leu Val  
 225 230 235 240  
 Val Glu Ile Pro Pro Phe Arg Asn Gln Arg Ile Thr Ser Pro Val His  
 245 250 255  
 Val Ser Phe Tyr Val Cys Asn Gly Lys Arg Lys Arg Ser Gln Tyr Gln  
 260 265 270  
 Arg Phe Thr Tyr Leu Pro Ala Asn Gly Asn Ala Ile Phe Leu Thr Val  
 275 280 285  
 Ser Arg Glu His Glu  
 290

<210> 52  
 <211> 293  
 <212> FRT  
 <213> Mouse

<400> 52  
 Pro Leu Ser Asn Gln Ser Gly Ser Tyr Glu Leu Arg Ile Glu Val Gln  
 1 5 10 15  
 Pro Lys Pro His His Arg Ala His Tyr Glu Thr Glu Gly Ser Arg Gly  
 20 25 30  
 Ala Val Lys Ala Pro Thr Gly Gly His Pro Val Val Gln Leu His Gly  
 35 40 45  
 Tyr Met Glu Asn Lys Pro Leu Gly Leu Gln Ile Phe Ile Gly Thr Ala  
 50 55 60  
 Asp Glu Arg Ile Leu Lys Pro His Ala Phe Tyr Gln Val His Arg Ile  
 65 70 75 80  
 Thr Gly Lys Thr Val Thr Thr Thr Ser Tyr Glu Lys Ile Val Gly Asn  
 85 90 95  
 Thr Lys Val Leu Glu Ile Pro Leu Glu Pro Lys Asn Asn Met Arg Ala  
 100 105 110

24

Thr Ile Asp Cys Ala Gly Ile Leu Lys Leu Arg Asn Ala Asp Ile Glu  
115 120 125

Leu Arg Lys Gly Glu Thr Asp Ile Gly Arg Lys Asn Thr Arg Val Arg  
130 135 140

Leu Val Phe Arg Val His Val Pro Glu Pro Ser Gly Arg Ile Val Ser  
145 150 155 160

Leu Gln Ala Ala Ser Asn Pro Ile Glu Cys Ser Gln Arg Ser Ala His  
165 170 175

Glu Leu Pro Met Val Glu Arg Gln Asp Met Asp Ser Cys Leu Val Tyr  
180 185 190

Gly Gly Gln Gln Met Ile Leu Thr Gly Gln Asn Phe Thr Ala Glu Ser  
195 200 205

Lys Val Val Phe Met Glu Lys Thr Thr Asp Gly Gln Gln Ile Trp Glu  
210 215 220

Met Glu Ala Thr Val Asp Lys Asp Lys Ser Gln Pro Asn Met Leu Phe  
225 230 235 240

Val Glu Ile Pro Glu Tyr Arg Asn Lys His Ile Arg Val Pro Val Lys  
245 250 255

Val Asn Phe Tyr Val Ile Asn Gly Lys Arg Lys Arg Ser Gln Pro Gln  
260 265 270

His Phe Thr Tyr His Pro Val Pro Ala Ile Lys Thr Glu Pro Ser Asp  
275 280 285

Glu Tyr Glu Pro Ser  
290

<210> 53  
<211> 11  
<212> DNA  
<213> Unknown

<220>  
<223> Description of Unknown Organism: enhancer capable  
of binding to an NF-AT complex

<400> 53  
aagaggaaaa a

11

<210> 54  
<211> 20  
<212> DNA  
<213> Unknown

<220>  
<223> Description of Unknown Organism: putative NF-AT  
binding site

<400> 54  
gaaaggagga aaaactgttt

20

25

<210> 55  
<211> 20  
<212> DNA  
<213> Unknown

<220>  
<223> Description of Unknown Organism: putative NF-AT  
binding site

<400> 55  
ccaaagagga aaattgttt

20

<210> 56  
<211> 20  
<212> DNA  
<213> Unknown

<220>  
<223> Description of Unknown Organism: putative NF-AT  
binding site

<400> 56  
cagaagagga aaaatgaag

20

<210> 57  
<211> 20  
<212> DNA  
<213> Unknown

<220>  
<223> Description of Unknown Organism: putative NF-AT  
binding site

<400> 57  
tccaggagaa aaaatgcctc

20

<210> 58  
<211> 20  
<212> DNA  
<213> Unknown

<220>  
<223> Description of Unknown Organism: putative NF-AT  
binding site

<220>  
<221> modified\_base  
<222> (9)  
<223> i

<400> 58  
aaaacttgng aaaatacgta

20

<210> 59  
<211> 20  
<212> DNA  
<213> Unknown

<220>  
<223> Description of Unknown Organism: putative NF-AT  
binding site

26

<400> 59  
taaaggagag aacaccagct

20

<210> 60  
<211> 20  
<212> DNA  
<213> Unknown

<220>  
<223> Description of Unknown Organism: putative NF-AT  
binding site

<400> 60  
gcaggggtggg aaaggccttt

20

<210> 61  
<211> 29  
<212> DNA  
<213> Unknown

<220>  
<223> Description of Unknown Organism: end-labeled  
binding site for NF-AT

<400> 61  
ggaggaaaaa ctgttcatac agaaggggt

29

<210> 62  
<211> 31  
<212> DNA  
<213> Unknown

<220>  
<223> Description of Unknown Organism: mutant NF-AT  
probe

<400> 62  
aagaaaggag taataattt ttaatacaga a

31